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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/081,969

DATE: 08/14/2002
TIME: 09:38:48

Input Set : A:\31704A.ST25.txt
Output Set: N:\CRF3\08142002\J081969.raw

3 <110> APPLICANT: Cheng, Cheng
4 Clarke, Lori
5 Connelly, Sheila
6 Ennist, David
7 Forry-Schaudies, Suzanne
8 Gorziglia, Mario
9 Hallenbeck, Paul
10 Hay, Carl
11 Jakubczak, John
12 Kaleko, Michael
13 Phipps, Sandrina
14 Police, Seshidhar
15 Ryan, Patricia
16 Steward, David
17 Xie, Yuefeng
19 <120> TITLE OF INVENTION: Novel Oncolytic Adenoviral Vectors
21 <130> FILE REFERENCE: 4-31704A/GTI
23 <140> CURRENT APPLICATION NUMBER: US 10/081,969
24 <141> CURRENT FILING DATE: 2002-02-22
26 <150> PRIOR APPLICATION NUMBER: US 60/270,922
27 <151> PRIOR FILING DATE: 2001-02-23
29 <150> PRIOR APPLICATION NUMBER: US 60/295,037
30 <151> PRIOR FILING DATE: 2001-06-01
32 <150> PRIOR APPLICATION NUMBER: US 60/348,670
33 <151> PRIOR FILING DATE: 2000-01-14
35 <160> NUMBER OF SEQ ID NOS: 98
37 <170> SOFTWARE: PatentIn version 3.1
39 <210> SEQ ID NO: 1
40 <211> LENGTH: 140
41 <212> TYPE: DNA
42 <213> ORGANISM: Simian virus 40
44 <220> FEATURE:
45 <221> NAME/KEY: misc_feature
46 <222> LOCATION: (1)..(140)
47 <223> OTHER INFORMATION:
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (1)..(140)
52 <223> OTHER INFORMATION: Fig. 1 A
55 <400> SEQUENCE: 1
56 cttatcgata cgcgcgaaac ttgtttattg cagccttataa tggttacaaa taaagcaaca 60
58 caaatttcac aaataaagca tttttttcac tgcattctag ttgtggtttg tccaaactca 120
60 tcaatgtatc ttatcatgtc 140

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63 <210> SEQ ID NO: 2
64 <211> LENGTH: 600
65 <212> TYPE: DNA
66 <213> ORGANISM: Human adenovirus type 5
68 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
70 <222> LOCATION: (1)..(600)
71 <223> OTHER INFORMATION: Fig. 2- E1A transcriton control region
74 <400> SEQUENCE: 2
75 catcatcaat aatatacctt attttgatt gaagccaata tgataatgag ggggtggagt      60
77 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagtagtgtg gcggaagtgt      120
79 gatgttgcaa gtgtggcgga acacatgtaa gcgacggatg tggcaaaagt gacgtttttg      180
81 gtgtgcgccg gtgtacacag gaagtgacaa ttttcgcgcg gttttaggcg gatgttgtag      240
83 taaatttggg cgtaaccgag taagatttgg ccattttcgc gggaaaactg aataagagga      300
85 agtgaaatct gaataatttt gtgttactca tagcgcgtaa tatttgtcta gggccgcggg      360
87 gactttgacc gtttacgttg agactcgccc aggtgttttt ctcaggtgtt ttccgcgttc      420
89 cgggtcaaag ttggcgtttt attattatag tcagctgacg tgtagtgtat ttatacccg      480
91 tgagttcctc aagaggccac tcttgagtgc cagcgagtag agttttctcc tccgagccgc      540
93 tccgacaccg ggactgaaaa tgagacatat tatctgccac ggaggtgtta ttaccgaaga      600
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 1802
98 <212> TYPE: DNA
99 <213> ORGANISM: artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: viral vector construct
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(1802)
107 <223> OTHER INFORMATION:
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (1)..(1802)
112 <223> OTHER INFORMATION: Fig. 3 A-Left end of Ar6pAE2fF sequence
115 <400> SEQUENCE: 3
116 catcatcaat aatatacctt attttgatt gaagccaata tgataatgag ggggtggagt      60
118 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcg tcaagcttat      120
120 cgataccgtc gaaacttggt tattgcagct tataatgggt acaaataaag caatagcatc      180
122 acaaatttca caaataaagc atttttttca ctgcattcta gttgtggttt gtccaaaactc      240
124 atcaatgtat cttatcatgt ctggatccgc gccgctagcg atcatccgga caaagcctgc      300
126 gcgcgccccg ccccgccatt ggccgtaccg ccccgcgccg ccgccccatc tcgcccctcg      360
128 ccgcccgggtc cggcgcggtta agccaatag gaaccgcccgc cgttgttccc gtcacggccg      420
130 gggcagccaa ttgtggcggc gctcgcggcg tcgtggctct ttcgcggcaa aaaggatttg      480
132 gcgcgtaaaa gtggccggga ctttgaggc agcgcgggcc gggggcgag cgggatcgag      540
134 ccctcgatga tatcagatca tcggatcccg gtcgactgaa aatgagacat attatctgcc      600
136 acggaggtgt tattaccgaa gaaatggccg ccagtccttt ggaccagctg atcgaagagg      660
138 tactggctga taatcttcca cctcctagcc attttgaacc acctaccctt cacgaactgt      720
140 atgattttaga cgtgacggcc cccgaagatc ccaacgagga ggcggtttcg cagatttttc      780
142 ccgactctgt aatgttggcg gtgcaggaag ggattgactt actcactttt ccgcccggcg      840
144 ccggttctcc ggagccgcct cacctttccc ggcagcccga gcagccggag cagagagcct      900

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146 tgggtccggt ttctatgcca aaccttgtac cggaggtgat cgatcttacc tgccacgagg      960
148 ctggctttcc acccagtgc gacgaggatg aagagggtga ggagtttgtg ttagattatg      1020
150 tggagcacc cgggcacggt tgcaggtctt gtcattatca ccggaggaat acgggggacc      1080
152 cagatattat gtgttcgctt tgctatatga ggacctgtgg catgtttgtc tacagtaagt      1140
154 gaaaattatg ggcagtgggt gatagagtgg tgggtttggt gtggtaatTT tttttttaat      1200
156 ttttacagtt ttgtggttta aagaattttg tattgtgatt tttttaaaag gtcctgtgtc      1260
158 tgaacctgag cctgagcccg agccagaacc ggagcctgca agacctaccc gccgtcctaa      1320
160 aatggcgccg gctatcctga gacgcccgc atcacctgtg tctagagaat gcaatagtag      1380
162 tacggatagc tgtgactccg gtccttctaa cacacctcct gagatacacc cggtggtccc      1440
164 gctgtgcccc attaaaccag ttgccgtgag agttgggtgg cgtcgccagg ctgtggaatg      1500
166 tatcgaggac ttgcttaacg agcctgggca accttgggac ttgagctgta aacgccccag      1560
168 gccataaggt gtaaacctgt gattgcgtgt gtggttaacg ctttgtttg ctgaatgagt      1620
170 tgatgtaagt ttaataaagg gtgagataat gtttaacttg catggcgtgt taaatggggc      1680
172 ggggcttaaa gggatatataa tgcgcgctgg gctaactctg gttacatctg acctcatgga      1740
174 ggcttgggag tgtttggaag atttttctgc tgtgcgtaac ttgctggaac agagctctaa      1800
176 ca                                                                                   1802

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179 <210> SEQ ID NO: 4

180 <211> LENGTH: 532

181 <212> TYPE: DNA

182 <213> ORGANISM: Artificial Sequence

184 <220> FEATURE:

185 <223> OTHER INFORMATION: Viral vector sequence

187 <220> FEATURE:

188 <221> NAME/KEY: misc_feature

189 <222> LOCATION: (1)..(532)

190 <223> OTHER INFORMATION: Fig. 3 B- right end of of Arp6AE2fF sequence

193 <400> SEQUENCE: 4

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194 aacctacgcc cagaaacgaa agccaaaaaa cccacaactt cctcaaatcg tcacttccgt      60
196 tttcccacgt tacgtcactt cccattttta ttaagaattc tacaattccc aacacataca      120
198 agttactccg ccctaaaacc ctgggcgagt ctccacgtaa acgggtcaaa tccccgcggc      180
200 cctagacaaa tattacgcgc tatgagtaac acaaaattat tcagatttca cttcctctta      240
202 ttcagttttc ccgcgaaaat ggccaaatct tactcggtta cgcccaaatt tactacaaca      300
204 tccgcctaaa accgcgcgaa aattgtcact tcctgtgtac accggcgcac accaaaaacg      360
206 tcacttttgc cacatccgtc gcttacatgt gttccgccac acttgcaaca tcacacttcc      420
208 gccacactac tacgtcaccc gccccgttcc cagcccccgc gccacgtcac aaactccacc      480
210 ccctcattat catattggct tcaatccaaa ataaggtata ttattgatga tg                    532

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213 <210> SEQ ID NO: 5

214 <211> LENGTH: 660

215 <212> TYPE: DNA

216 <213> ORGANISM: Artificial Sequence

218 <220> FEATURE:

219 <223> OTHER INFORMATION: Viral vector construct

221 <220> FEATURE:

222 <221> NAME/KEY: misc_feature

223 <222> LOCATION: (1)..(660)

224 <223> OTHER INFORMATION: Fig. 4-Left end of Ar6F sequence

227 <400> SEQUENCE: 5

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228 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt      60
230 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcg cgtacgcgat      120

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232 atcggatccc ggtcgactga aaatgagaca tattatctgc cacggagggtg ttattaccga      180
234 agaaatggcc gccagtcttt tggaccagct gatcgaagag gtactggctg ataatcttcc      240
236 acctcctagc cattttgaac cacctaccct tcacgaactg tatgatttag acgtgacggc      300
238 ccccggaagat cccaacgagg aggcgggtttc gcagattttt cccgactctg taatgttggc      360
240 ggtgcaggaa gggattgact tactcacttt tccgccggcg cccggttctc cggagccgcc      420
242 tcacctttcc cggcagcccg agcagccgga gcagagagcc ttgggtccgg tttctatgcc      480
244 aaaccttgta cgggagggtga tcgatcttac ctgccacgag gctggctttc caccagtgta      540
246 cgacgaggat gaagagggtg aggagtttgt gttagattat gtggagcacc ccgggcacgg      600
248 ttgcagggtct tgtcattatc accggaggaa tacggggggac ccagatatta tgtgttcgct      660
251 <210> SEQ ID NO: 6
252 <211> LENGTH: 660
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Fig. 5- left end of Ar6pAF sequence
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
261 <222> LOCATION: (1)..(660)
262 <223> OTHER INFORMATION: Fig. 5- left end of Ar6pAF sequence
265 <400> SEQUENCE: 6
266 catcatcaat aatatacctt attttggatt gaagccaata tgataatgag ggggtggagt      60
268 ttgtgacgtg gcgcggggcg tgggaacggg gcgggtgacg tagggcgcgga tcaagcttat      120
270 cgataccgtc gaaacttggt tattgcagct tataatggtt acaaataaag caatagcatc      180
272 acaaatttca caaataaagc atttttttca ctgcattcta gttgtggttt gtccaaactc      240
274 atcaatgtat cttatcatgt ctggatccgc gccgctagcg atatcggatc ccggtcgact      300
276 gaaaatgaga catattatct gccacggagg tgttattacc gaagaaatgg ccgccagtct      360
278 tttggaccag ctgatcgaag aggtactggc tgataatctt ccacctccta gccattttga      420
280 accacctacc cttcacgaac tgtatgattt agacgtgacg gccccgaag atcccaacga      480
282 ggaggcgggt tcgcagattt ttcccgactc tgtaatgttg gcggtgcagg aagggttgta      540
284 cttactcact ttccgcgcgg cgcccggttc tccggagccg cctcaccttt cccggcagcc      600
286 cgagcagccg gagcagagag ccttgggtcc gttttctatg ccaaaccttg taccggaggt      660
289 <210> SEQ ID NO: 7
290 <211> LENGTH: 949
291 <212> TYPE: DNA
292 <213> ORGANISM: Murine
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (182)..(640)
297 <223> OTHER INFORMATION:
299 <400> SEQUENCE: 7
300 ttccggacag acctcaataa ctctgtttac cagaacagga ggtgagctta gaaaaccctt      60
302 agggatttag gccaaaggcg cagctactgt ggggtttatg aacaattcaa gcaactctac      120
304 gggctattct aattcaggtt tctctagccg ggctgcagga attcgatggc cgctacctac      180
306 a atg gcc cac gag aga aag gct aag gtc ctg agg agg atg tgg ctg cag      229
307 Met Ala His Glu Arg Lys Ala Lys Val Leu Arg Arg Met Trp Leu Gln
308 1 5 10 15
310 aat tta ctt ttc ctg ggc att gtg gtc tac agc ctc tca gca ccc acc      277
311 Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu Ser Ala Pro Thr
312 20 25 30

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314 cgc tca ccc atc act gtc acc cgg cct tgg aag cat gta gag gcc atc      325
315 Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val Glu Ala Ile
316          35                      40                      45
318 aaa gaa gcc ctg aac ctc ctg gat gac atg cct gtc aca ttg aat gaa      373
319 Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr Leu Asn Glu
320          50                      55                      60
322 gag gta gaa gtc gtc tct aac gag ttc tcc ttc aag aag cta aca tgt      421
323 Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys Leu Thr Cys
324 65          70                      75                      80
326 gtg cag acc cgc ctg aag ata ttc gag cag ggt cta cgg ggc aat ttc      469
327 Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg Gly Asn Phe
328          85                      90                      95
330 acc aaa ctc aag ggc gcc ttg aac atg aca gcc agc tac tac cag aca      517
331 Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr
332          100                     105                     110
334 tac tgc ccc cca act ccg gaa acg gac tgt gaa aca caa gtt acc acc      565
335 Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr
336          115                     120                     125
338 tat gcg gat ttc ata gac agc ctt aaa acc ttt ctg act gat atc ccc      613
339 Tyr Ala Asp Phe Ile Asp Ser Leu Lys Thr Phe Leu Thr Asp Ile Pro
340          130                     135                     140
342 ttt gaa tgc aaa aaa cca gtc caa aaa tgaggaagcc caggccagct      660
343 Phe Glu Cys Lys Lys Pro Val Gln Lys
344 145                     150
346 ctgaatccag cttctcagac tgctgctttt gtgcctgcgt aatgagccag gaactcggaa      720
348 tttctgcctt aaagggacca agagatgtgg cacaggtagt cgaatcaagc ttatcgatac      780
350 cgtcgacctc gactagataa cttcgtataa tgtatgctat acgaagtatt gctagaaatg      840
352 gacggaatta ttacagagca gcgcctgcta gaaagacgca gggcagcggc cgagcaacag      900
354 cgcatgaatc aagagctcca agacatggtt aacttgcacc agtgcaaaa      949
357 <210> SEQ ID NO: 8
358 <211> LENGTH: 153
359 <212> TYPE: PRT
360 <213> ORGANISM: Murine
362 <400> SEQUENCE: 8
364 Met Ala His Glu Arg Lys Ala Lys Val Leu Arg Arg Met Trp Leu Gln
365 1          5                      10                      15
368 Asn Leu Leu Phe Leu Gly Ile Val Val Tyr Ser Leu Ser Ala Pro Thr
369          20                      25                      30
372 Arg Ser Pro Ile Thr Val Thr Arg Pro Trp Lys His Val Glu Ala Ile
373          35                      40                      45
376 Lys Glu Ala Leu Asn Leu Leu Asp Asp Met Pro Val Thr Leu Asn Glu
377          50                      55                      60
380 Glu Val Glu Val Val Ser Asn Glu Phe Ser Phe Lys Lys Leu Thr Cys
381 65          70                      75                      80
384 Val Gln Thr Arg Leu Lys Ile Phe Glu Gln Gly Leu Arg Gly Asn Phe
385          85                      90                      95
388 Thr Lys Leu Lys Gly Ala Leu Asn Met Thr Ala Ser Tyr Tyr Gln Thr
389          100                     105                     110
392 Tyr Cys Pro Pro Thr Pro Glu Thr Asp Cys Glu Thr Gln Val Thr Thr

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VERIFICATION SUMMARY

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